```
                                    ┌── LIBRARY 1
                   SEQUENCES ───────┼── LIBRARY 2
                                    └── LIBRARY "N"

                                    ┌── LIBRARY 1
                   TRIMMED ─────────┼── LIBRARY 2
                                    └── LIBRARY "N"

                                    ┌── LIBRARY 1
                   TRIMPARS ────────┼── LIBRARY 2
                                    └── LIBRARY "N"

                                    ┌── LIBRARY 1
                   HTML ────────────┼── LIBRARY 2
                                    └── LIBRARY "N"

    ROOT ──┤                        ┌── LIBRARY 1
                   EXCEL ───────────┼── LIBRARY 2
                                    └── LIBRARY "N"

                                    ┌── LIBRARY 1.XLS (FILE)
                   LIBRARY ─────────┼── LIBRARY 2.XLS (FILE)
                                    └── LIBRARY "N".XLS (FILE)

                   VECTORS

                   TEMP
```

FIG−1

Subtraction Library Utility
? ☐ ☒

Choose the desired utility function

⦿ Select a Library

Known Subtraction Libraries

Create New
Library and
Associated
Directories

| ralph |
| test |
| test1 |

○ Trim raw sequences

Known
Vector Files:

PCR-SELECT PRIMERS

Threshold: 80

○ Blast trimmed sequences

Available Databases to be searched

☐ est   ☐ yeast   ☐ htgs   ☐ vector
☒ nr   ☐ ecoli   ☐ pdb   ☒ kabat
☐ month   ☐ sts   ☐ alu   ☐ epd

Descriptions: 20

Alignments: 20

○ Create XLS files from blasted (HTML) sequence files

○ Update library from selected XLS files

Exit

Help

Select Files

0   files will be
    processed

Go

Blast Later

☒ Sound

☒ Help Tips

Minimize

FIG-2

Confirm or Enter Trimming Positions

Insertion Orientation

	Starting or 5' Adapter/Vector Information		
	Sequence	Score	#
Positive	AGCGGCCGCCCGGGCCAGGT	68%	0 0
Negative	AGCGTGGTCGCGGCCGAGGT	100%	0 0

	Ending or 3' Adapter/Vector Information		
	Sequence	Score	#
	ACCTCGGCCGCGGGACCACGCT	70%	0 0
	ACCTGCCCGGGCGGCCGCT	100%	0 0

TTAGCCGTGGTCGCGGCCGAGGTACAGAGAACACTGACAAACAAGCAAGGAAGACGGCGCAGAGAAAGAAGAAAGACCTAGAAAGGTTGTAGATGGAAATCAGGAATGATTTGAACTGATAAAGATTTCGGA
CTCATAAGAACACAGCATTTTAAAATGTTAAACACAAAAACTACTGACTGAAGATAGAAGAAGAATGCGATGGATTTTATTACACATGGTGGAAGAGAAGAGAGGCGTGTAGGTTTGCAAACAAA
GTTAAGAAAATAGGAAACTGAATTTTCATTGTACAGAAAATGTATCTTCTTGGGGAAGGCCTGTGTACCTGCCCGGGCGGCCGCTGTGAAATTCCAGCACACTGGCGGCCGTTACTAGTGGATCC
CANCTCGGTACCAAGCTTGGGTATCATGGTCNTAANCTGTTCCTGTGTGAAATTGTTATCCNCNCNCCCCCATTCCCCCCACNTTCCAACCCGAAACCTTAAATTTTTAACCNCAGGTGCCN
AATGAATNACCCACCCCNTTATGCTTTGCCNCCTGCCCCTTCCNTCGGAACNTCNCCCCTCTTTNTAAACCGNCNCCCCNGGAAAGCGTTTCTTTTGGCCCCTCCCCTCNCCCCCTCCTNAT
CCTGCCCCT

5'
3'

\\Mricd-fs1\sweeneyre\Sub Lib Test\Sequence\test\41k06.seq

Remove below base: 23	Length: 289	Confirm Fwd: TTACTAGTGGATCCGGAGCTCGGTACCAAGCTT	0%
Remove above base: 312	Threshold: 80	Confirm Rev: TTCGAACCATGGCTCGAGCC	0%

☐ Allow Inserts ☐ Positive Orientation
☑ Allow Deletes ☑ Use Threshold

Find Best

Sequencing direction was not determined

The current sequence was previously trimmed

Back   Apply   Skip   Abort All

10 12 14 16

FIG-3